

SEQUENCE LISTING

<110> Sundelin, Johan  
Scarborough, Robert M.

<120> Recombinant C140 Receptor, Its Agonists and Antagonists, and  
Nucleic Acids Encoding the Receptor

<130> 44481-5006-09-US

<140> US 10/127,691  
<141> 2002-04-23

<150> US 08/097,938  
<151> 1993-07-26

<150> US 08/390,301  
<151> 1995-01-25

<150> US 08/474,414  
<151> 1995-06-07

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<170> PatentIn Ver. 2.1

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acacaagaat tagacttcaa ccgtcaccaa ctgccctgtg taggacggtc ggtcaactgaa 180  
agagaatatt gtctgcaata ctctaatgac atctgtctgt gttcatctga a atg ttc 237  
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Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile Thr Gly Lys Gly  
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gcc tac gtg ctc atg atc aag acg ctc cgc tct tct gct atg gat gaa Ala Tyr Val Leu Met Ile Lys Thr Leu Arg Ser Ser Ala Met Asp Glu 260 265 270	1053
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325                           330                           335				
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agc tca acc agt gtt aaa acc tcc tac tgagctgtac ctgaggatgt Ser Ser Thr Ser Val Lys Thr Ser Tyr				1436
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 Asn Pro Met Gly His Pro Arg Lys Lys Ala Asn Ile Ala Val Gly Val  
 180 185 190  
 Ser Leu Ala Ile Trp Leu Leu Ile Phe Leu Val Thr Ile Pro Leu Tyr  
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 Val Met Lys Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr Thr Cys  
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 His Asp Val Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe Asn Tyr  
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 Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Leu Leu Thr  
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 Ala Ser Ala Tyr Val Leu Met Ile Lys Thr Leu Arg Ser Ser Ala Met  
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 Asp Glu His Ser Glu Lys Lys Arg Gln Arg Ala Ile Arg Leu Ile Ile  
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 Thr Val Leu Ala Met Tyr Phe Ile Cys Phe Ala Pro Ser Asn Leu Leu  
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 Ala Arg Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Asn Arg Met  
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tct gta atg acc ctt gtc ttc ctt tct tgt aca gga acc aat aga tcc 154  
Ser Val Met Thr Leu Val Phe Leu Ser Cys Thr Gly Thr Asn Arg Ser  
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tct aaa gga aga agc ctt att ggt aag gtt gat ggc aca tcc cac gtc 202  
Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val  
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act gga aaa gga gtt aca gtt gaa aca gtc ttt tct gtg-gat gag ttt 250  
Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe  
50 55 60 65  
  
tct gca tct gtc ctc act gga aaa ctg acc act gtc ttc ctt cca att 298  
Ser Ala Ser Val Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Ile  
70 75 80  
  
gtc tac aca att gtg ttt gtg gtg ggt ttg cca agt aac ggc atg gcc 346  
Val Tyr Thr Ile Val Phe Val Val Gly Leu Pro Ser Asn Gly Met Ala  
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Leu Trp Val Phe Leu Phe Arg Thr Lys Lys His Pro Ala Val Ile  
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Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe  
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Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr Gly  
130 135 140 145  
  
gaa gct ctt tgt aat gtg ctt att ggc ttt ttc tat ggc aac atg tac 538  
Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr  
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tgt tcc att ctc ttc atg acc tgc ctc agt gtg cag'agg tat tgg gtc 586  
Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val  
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Phe	Pro	Leu	Lys	Ile	Ala	Tyr	His	Ile	His	Gly	Asn	Asn	Trp	Ile	Tyr
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Gly	Glu	Ala	Leu	Cys	Asn	Val	Leu	Ile	Gly	Phe	Phe	Tyr	Gly	Asn	Met
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Lys	Gln	Met	Gln	Val	Ser	Leu	Thr	Ser	Lys	Lys	His	Ser	Arg	Lys	Ser
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Lys Gly Val Pro Val Glu Pro Gly Phe Ser Ile Asp Glu Phe Ser Ala  
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Ser Ile Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Val Val Tyr  
 65 70 75 80

Ile Ile Val Phe Val Ile Gly Leu Pro Ser Asn Gly Met Ala Leu Trp  
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Ile Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile Tyr Met  
100 105 110

Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe Pro Leu  
115 120 125

Lys Ile Ser Tyr His Leu His Gly Asn Asn Trp Val Tyr Gly Glu Ala  
130 135 140

Leu Cys Lys Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr Cys Ser  
145 150 155 160

Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val Ile Val  
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 Asn Pro Met Gly His Pro Arg Lys Lys Ala Asn Ile Ala Val Gly Val  
 180 185 190  
 Ser Leu Ala Ile Trp Leu Leu Ile Phe Leu Val Thr Ile Pro Leu Tyr  
 195 200 205  
 Val Met Lys Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr Thr Cys  
 210 215 220  
 His Asp Val Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe Asn Tyr  
 225 230 235 240  
 Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Leu Leu Thr  
 245 250 255  
 Ala Ser Ala Tyr Val Leu Met Ile Lys Thr Leu Arg Ser Ser Ala Met  
 260 265 270  
 Asp Glu His Ser Glu Lys Lys Arg Gln Arg Ala Ile Arg Leu Ile Ile  
 275 280 285  
 Thr Val Leu Ala Met Tyr Phe Ile Cys Phe Ala Pro Ser Asn Leu Leu  
 290 295 300  
 Leu Val Val His Tyr Phe Leu Ile Lys Thr Gln Arg Gln Ser His Val  
 305 310 315 320  
 Tyr Ala Leu Tyr Leu Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys  
 325 330 335  
 Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser Lys Asp Phe Arg Asp His  
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 Ala Arg Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Asn Arg Met  
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 Ile Gly Ile Ser Leu Ala Ile Trp Leu Leu Ile Leu Val Thr Ile  
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 Ser Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys  
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 Leu Ile Val Thr Val Leu Ala Met Tyr Leu Ile Cys Phe Ile Pro Ser  
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 Ser His Val Tyr Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu  
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Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe  
340 345 350

Arg Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val  
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Ser Ser Tyr Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr  
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35 40 45

Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser  
50 55 60

Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu  
65 70 75 80

Gln Lys Gln Leu Pro Ala Phe Ile Ser Glu Asp Ala Ser Gly Tyr Leu  
85 90 95

Thr Ser Ser Trp Leu Thr Leu Phe Val Pro Ser Val Tyr Thr Gly Val  
100 105 110

Phe Val Val Ser Leu Pro Leu Asn Ile Met Ala Ile Val Val Phe Ile  
115 120 125

Leu Lys Met Lys Val Lys Lys Pro Ala Val Val Tyr Met Leu His Leu  
130 135 140

Ala Thr Ala Asp Val Leu Phe Val Ser Val Leu Pro Phe Lys Ile Ser  
145 150 155 160

Tyr Tyr Phe Ser Gly Ser Asp Trp Gln Phe Gly Ser Glu Leu Cys Arg  
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Met Thr Val Ile Ser Ile Asp Arg Phe Leu Ala Val Val Tyr Pro Met  
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 Cys Tyr Val Ser Ile Ile Arg Cys Leu Ser Ser Ala Val Ala Asn  
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 Arg Ser Lys Lys Ser Arg Ala Leu Phe Leu Ser Ala Ala Val Phe Cys  
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 325   330   335  
  
 Tyr Ser Phe Leu Ser His Thr Ser Thr Thr Glu Ala Ala Tyr Phe Ala  
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 Tyr Leu Leu Cys Val Cys Val Ser Ser Ile Ser Ser Cys Ile Asp Pro  
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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor antagonist

<220>  
<221> VARIANT  
<222> (1)..(2)  
<223> Xaa at position 1 = 3-mercaptopropionic acid; Xaa at position 2 = cyclohexylalanine

<400> 11  
Xaa Xaa Leu Lys Gly  
1 5

<210> 12

<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor antagonist

<220>  
<221> VARIANT  
<222> (1)..(2)  
<223> Xaa at position 1 = 3-mercaptopropionic acid; Xaa at position 2 = cyclohexylalanine

<400> 12  
Xaa Xaa Ile Gly Arg  
1 5

<210> 13  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor antagonist

<220>  
<221> VARIANT  
<222> (1)  
<223> Xaa at position 1 = 3-mercaptopropionic acid

<400> 13  
Xaa Leu Leu Gly Lys Lys  
1 5

<210> 14  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor antagonist

<220>  
<221> VARIANT  
<222> (1)  
<223> Xaa at position 1 = 3-mercaptopropionic acid

<400> 14  
Xaa Leu Ile Gly Arg Lys  
1 5

<210> 15  
<211> 10

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor antagonist

<220>  
<221> VARIANT  
<222> (1)  
<223> Xaa at position 1 = 3-mercaptopropionic acid

<400> 15  
Xaa Leu Ile Gly Arg Lys Glu Thr Gln Pro  
1 5 10

<210> 16  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor antagonist

<220>  
<221> VARIANT  
<222> (1)  
<223> Xaa at position 1 = 3-mercaptopropionic acid

<400> 16  
Xaa Leu Leu Gly Lys Lys Asp Gly Thr Ser  
1 5 10

<210> 17  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor antagonist

<220>  
<221> VARIANT  
<222> (1)  
<223> Xaa at position 1 = (n-pentyl) 2-N-Leu

<400> 17  
Xaa Ile Gly Arg Lys  
1 5

<210> 18  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor antagonist

<220>  
<221> VARIANT  
<222> (1)  
<223> Xaa at position 1 = Me-N-(n-pentyl)

<400> 18  
Xaa Leu Ile Gly Arg Lys  
1 5

<210> 19  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor agonist/immunogen

<400> 19  
Ser Lys Gly Arg Ser Leu Ile Gly Arg Leu Glu Thr  
1 5 10

<210> 20  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor agonist/immunogen

<400> 20  
Ile Ser Tyr His Leu His Gly Asn Asn Trp Val Tyr Gly Glu Ala Leu  
1 5 10 15

Cys

<210> 21  
<211> 31  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor agonist/immunogen

<400> 21  
Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr Thr Cys His Asp Val  
1 5 10 15

Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe Asn Tyr Phe Leu  
20 25 30

<210> 22  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist/immunogen

<400> 22  
His Tyr Phe Leu Ile Lys Thr Gln Arg Gln Ser His Val Tyr Ala  
1 5 10 15

<210> 23  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 23  
Ser Leu Ile Gly Arg Leu  
1 5

<210> 24  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 24  
Ser Leu Ile Gly Arg Ala  
1 5

<210> 25  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 25  
Ser Leu Ile Gly Ala Leu  
1 5

<210> 26  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 26  
Ser Leu Ile Ala Arg Leu  
1 5

<210> 27  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 27  
Ser Leu Ala Gly Arg Leu  
1 5

<210> 28  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 28  
Ser Ala Ile Gly Arg Leu  
1 5

<210> 29  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 29  
Ala Leu Ile Gly Arg Leu  
1 5

<210> 30  
<211> 6

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 30  
Ser Phe Phe Leu Arg Trp  
1 5

<210> 31  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 31  
Arg Asn Asn Ser Ser Lys Gly Arg  
1 5

<210> 32  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 32  
Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile Thr  
1 5 10

<210> 33  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 33  
Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile  
1 5 10

<210> 34  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 34  
Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro  
1 5 10

<210> 35  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 35  
Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro  
1 5 10

<210> 36  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 36  
Ser Leu Ile Gly Arg Leu Glu Thr Gln  
1 5

<210> 37  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 agonist

<400> 37  
Ser Leu Ile Gly Arg Leu Glu Thr  
1 5

<210> 38  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 38  
Ser Leu Ile Gly Arg Leu Glu  
1 5

<210> 39  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 39  
Ser Leu Ile Gly Arg Leu  
1 5

<210> 40  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 40  
Ser Leu Ile Gly Arg  
1 5

<210> 41  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 41  
Ser Leu Leu Gly Lys Val Asp Gly Thr Ser His Val Thr  
1 5 10

<210> 42  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 42  
Ser Leu Leu Gly Lys Val Asp Gly Thr Ser His Val  
1 5 10

<210> 43  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor agonist

<400> 43  
Ser Leu Leu Gly Lys Val Asp Gly Thr Ser His  
1 5 10

<210> 44  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor agonist

<400> 44  
Ser Leu Leu Gly Lys Val Asp Gly Thr Ser  
1 5 10

<210> 45  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor agonist

<400> 45  
Ser Leu Leu Gly Lys Val Asp Gly Thr  
1 5

<210> 46  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor agonist

<400> 46  
Ser Leu Leu Gly Lys Val Asp Gly  
1 5

<210> 47

<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor agonist

<400> 47  
Ser Leu Leu Gly Lys Val Asp  
1 5

<210> 48  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor agonist

<400> 48  
Ser Leu Leu Gly Lys Val  
1 5

<210> 49  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor agonist

<400> 49  
Ser Leu Leu Gly Lys  
1 5

<210> 50  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor agonist

<220>  
<221> VARIANT  
<222> (2)  
<223> Xaa at position 2 = cyclohexylalanine (Cha)

<400> 50  
Ser Xaa Ile Gly Arg  
1 5

<210> 51  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor agonist

<220>  
<221> VARIANT  
<222> (2)  
<223> Xaa at position 2 = cyclohexylalanine (Cha)

<400> 51  
Ser Xaa Leu Gly Lys  
1 5

<210> 52  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor agonist

<220>  
<221> VARIANT  
<222> (1)  
<223> Xaa at position 1 = 2,3-diamino propionic acid (2,3-diaP)

<400> 52  
Xaa Ile Gly Arg  
1

<210> 53  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor agonist

<220>  
<221> VARIANT  
<222> (1)  
<223> Xaa at position 1 = 2,3-diamino propionic acid (2,3-diaP)

<400> 53  
Xaa Leu Leu Gly Lys  
1 5

<210> 54  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 54  
Ser Leu Leu Gly Lys Arg  
1 5

<210> 55  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<400> 55  
Ser Leu Ile Gly Arg Arg  
1 5

<210> 56  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<220>  
<221> VARIANT  
<222> (2)  
<223> Xaa at position 2= cyclohexylalanine (Cha)

<400> 56  
Ser Xaa Leu Gly Lys Lys  
1 5

<210> 57  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 agonist  
receptor

<220>  
<221> VARIANT

<222> (2)  
<223> Xaa at position 2 = cyclohexylalanine (Cha)

<400> 57  
Ser Xaa Ile Gly Arg Lys  
1 5

<210> 58  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<220>  
<221> VARIANT  
<222> (1)  
<223> Xaa at position 1 = 2,3-diamino propionic acid  
(2,3-diaP)

<400> 58  
Xaa Leu Ile Gly Arg Lys  
1 5

<210> 59  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: C140 receptor  
agonist

<220>  
<221> VARIANT  
<222> (1)  
<223> Xaa at position 1 = 2,3-diamino propionic acid  
(2,3-diaP)

<400> 59  
Xaa Leu Leu Gly Lys Lys  
1 5

<210> 60  
<211> 2732  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (73)...(1269)  
<223> C140 receptor, cDNA and deduced protein sequences

<400> 60

ccctgtgctc agagtagggc tccgagttc gaaccactgg tggcggattg cccgcccc 60  
 ccacgtccgg gg atg cga agt ctc agc ctg gcg tgg ctg ctg gga ggt atc 111  
     Met Arg Ser Leu Ser Leu Ala Trp Leu Leu Gly Gly Ile  
     1                 5                             10  
  
 acc ctt ctg gcg gcc tcg gtc tcc tgc agc cg<sup>g</sup> acc gag aac ctt gca 159  
   Thr Leu Leu Ala Ala Ser Val Ser Cys Ser Arg Thr Glu Asn Leu Ala  
   15                 20                             25  
  
 ccg gga [cg<sup>c</sup> aac aac agt aaa gga aga] agt ctt att ggc aga tta gaa 207  
   Pro Gly [Arg Asn Asn Ser Lys Gly Arg] Ser Leu Ile Gly Arg Leu Glu  
   30                 35                             40                             45  
  
 acc cag cct cca atc act ggg aaa ggg gtt ccg gta gaa cca ggc ttt 255  
   Thr Gln Pro Pro Ile Thr Gly Lys Gly Val Pro Val Glu Pro Gly Phe  
   50                 55                             60  
  
 tcc atc gat gag ttc tct gcg tcc atc ctc acc ggg aag ctg acc acg 303  
   Ser Ile Asp Glu Phe Ser Ala Ser Ile Leu Thr Gly Lys Leu Thr Thr  
   65                 70                             75  
  
 gtc ttt ctt ccg gtc gtc tac att att gtg ttt gtg att ggt ttg ccc 351  
   Val Phe Leu Pro Val Val Tyr Ile Val Phe Val Ile Gly Leu Pro  
   80                 85                             90  
  
 agt aat ggc atg gcc ctc tgg atc ttc ctt ttc cga acg aag aag aaa 399  
   Ser Asn Gly Met Ala Leu Trp Ile Phe Leu Phe Arg Thr Lys Lys Lys  
   95                 100                             105  
  
 cac ccc gcc gtg att tac atg gcc aac ctg gcc ttg gcc gac ctc ctc 447  
   His Pro Ala Val Ile Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu  
   110                 115                             120                             125  
  
 tct gtc atc tgg ttc ccc ctg aag atc tcc tac cac cta cat ggc aac 495  
   Ser Val Ile Trp Phe Pro Leu Lys Ile Ser Tyr His Leu His Gly Asn  
   130                 135                             140  
  
 aac tgg gtc tac ggg gag gcc ctg tgc aag gtg ctc att ggc ttt ttc 543  
   Asn Trp Val Tyr Gly Glu Ala Leu Cys Lys Val Leu Ile Gly Phe Phe  
   145                 150                             155  
  
 tat ggt aac atg tat tgc tcc atc ctc ttc atg acc tgc ctc agc gtg 591  
   Tyr Gly Asn Met Tyr Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val  
   160                 165                             170  
  
 cag agg tac tgg gtg atc gtg aac ccc atg gga cac ccc agg aag aag 639  
   Gln Arg Tyr Trp Val Ile Val Asn Pro Met Gly His Pro Arg Lys Lys  
   175                 180                             185  
  
 gca aac atc gcc gtt ggc gtc tcc ttg gca atc tgg ctc ctg att ttt 687  
   Ala Asn Ile Ala Val Gly Val Ser Leu Ala Ile Trp Leu Leu Ile Phe  
   190                 195                             200                             205  
  
 ctg gtc acc atc cct ttg tat gtc atg aag cag acc atc tac att cca 735  
   Leu Val Thr Ile Pro Leu Tyr Val Met Lys Gln Thr Ile Tyr Ile Pro  
   210                 215                             220  
  
 gca ttg aac atc acc acc tgt cac gat gtg ctg cct gag gag gta ttg 783

Ala Leu Asn Ile Thr Thr Cys His Asp Val Leu Pro Glu Glu Val Leu			
225	230	235	
gtg ggg gac atg ttc aat tac ttc ctc tca ctg gcc att gga gtc ttc	831		
Val Gly Asp Met Phe Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe			
240	245	250	
ctg ttc ccg gcc ctc ctt act gca tct gcc tac gtg ctc atg atc aag	879		
Leu Phe Pro Ala Leu Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Lys			
255	260	265	
acg ctc cgc tct tct gct atg gat gaa cac tca gag aag aaa agg cag	927		
Thr Leu Arg Ser Ser Ala Met Asp Glu His Ser Glu Lys Lys Arg Gln			
270	275	280	285
agg gct atc cga ctc atc acc gtg ctg gcc atg tac ttc atc tgc	975		
Arg Ala Ile Arg Leu Ile Ile Thr Val Leu Ala Met Tyr Phe Ile Cys			
290	295	300	
ttt gct cct agc aac ctt ctg ctc gta gtg cat tat ttc cta atc aaa	1023		
Phe Ala Pro Ser Asn Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys			
305	310	315	
acc cag agg cag agc cac gtc tac gcc ctc tac ctt gtc gcc ctc tgc	1071		
Thr Gln Arg Gln Ser His Val Tyr Ala Leu Tyr Leu Val Ala Leu Cys			
320	325	330	
ctg tcg acc ctc aac agc tgc ata gac ccc ttt gtc tat tac ttt gtc	1119		
Leu Ser Thr Leu Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val			
335	340	345	
tca aaa gat ttc agg gat cac gcc aga aac gcg ctc ctc tgc cga agt	1167		
Ser Lys Asp Phe Arg Asp His Ala Arg Asn Ala Leu Leu Cys Arg Ser			
350	355	360	365
gtc cgc act gtg aat cgc atg caa atc tcg ctc agc tcc aac aag ttc	1215		
Val Arg Thr Val Asn Arg Met Gln Ile Ser Leu Ser Ser Asn Lys Phe			
370	375	380	
tcc agg aag tcc ggc tcc tac tct tca agc tca acc agt gtt aaa acc	1263		
Ser Arg Lys Ser Gly Ser Tyr Ser Ser Ser Thr Ser Val Lys Thr			
385	390	395	
tcc tac tgagctgtac ctgaggatgt caagcctgct tgatgatgtat gatgatgtat	1319		
Ser Tyr			
gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gcacccgtgt gtgagtgagt	1379		
ggtagggata caccaacatg gatggggctg tcatttctta tccaagctgt ctgtctctgc	1439		
accaatcaca agcatgcagc tctccccagg attgacagaa gcctcctcct ttgcatgaga	1499		
acagtcttcc actctgtatga aaagcatcag tatcagaaac taaaacgaac tgagaggagc	1559		
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acaaaaacta cacctggcaa gaaggctaag actctctgaa atgcttccct tttccatctg	1679		
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gactttacag acttgagaga ggagtgaatg aggagtgaat gaggctcctg gcggcatcct 1799  
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caccatttca tcagaactat tggggatctt gatcaatgtg caggtccctt agcgtcagta 1919  
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cttggatca gttttgttca ctaatttgc caataatgga attaacgtct tctcatctgt 2579  
ttgaggaaga tctgaaacaa ggggccattg caggagtaca tggctccagg cttactttat 2639  
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<210> 61  
<211> 399  
<212> PRT  
<213> *Mus musculus*

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Ala Ala Ser Val Ser Cys Ser Arg Thr Glu Asn Leu Ala Pro Gly Arg
      20          25          30

Asn Asn Ser Lys Gly Arg Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro
      35          40          45

Pro Ile Thr Gly Lys Gly Val Pro Val Glu Pro Gly Phe Ser Ile Asp
      50          55          60

Glu Phe Ser Ala Ser Ile Leu Thr Gly Lys Leu Thr Thr Val Phe Leu
      65          70          75          80

Pro Val Val Tyr Ile Ile Val Phe Val Ile Gly Leu Pro Ser Asn Gly
      85          90          95

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Met Ala Leu Trp Ile Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala  
 100 105 110  
 Val Ile Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile  
 115 120 125  
 Trp Phe Pro Leu Lys Ile Ser Tyr His Leu His Gly Asn Asn Trp Val  
 130 135 140  
 Tyr Gly Glu Ala Leu Cys Lys Val Leu Ile Gly Phe Phe Tyr Gly Asn  
 145 150 155 160  
 Met Tyr Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr  
 165 170 175  
 Trp Val Ile Val Asn Pro Met Gly His Pro Arg Lys Lys Ala Asn Ile  
 180 185 190  
 Ala Val Gly Val Ser Leu Ala Ile Trp Leu Leu Ile Phe Leu Val Thr  
 195 200 205  
 Ile Pro Leu Tyr Val Met Lys Gln Thr Ile Tyr Ile Pro Ala Leu Asn  
 210 215 220  
 Ile Thr Thr Cys His Asp Val Leu Pro Glu Glu Val Leu Val Gly Asp  
 225 230 235 240  
 Met Phe Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro  
 245 250 255  
 Ala Leu Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Lys Thr Leu Arg  
 260 265 270  
 Ser Ser Ala Met Asp Glu His Ser Glu Lys Lys Arg Gln Arg Ala Ile  
 275 280 285  
 Arg Leu Ile Ile Thr Val Leu Ala Met Tyr Phe Ile Cys Phe Ala Pro  
 290 295 300  
 Ser Asn Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Thr Gln Arg  
 305 310 315 320  
 Gln Ser His Val Tyr Ala Leu Tyr Leu Val Ala Leu Cys Leu Ser Thr  
 325 330 335  
 Leu Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser Lys Asp  
 340 345 350  
 Phe Arg Asp His Ala Arg Asn Ala Leu Leu Cys Arg Ser Val Arg Thr  
 355 360 365  
 Val Asn Arg Met Gln Ile Ser Leu Ser Ser Asn Lys Phe Ser Arg Lys  
 370 375 380  
 Ser Gly Ser Tyr Ser Ser Ser Ser Thr Ser Val Lys Thr Ser Tyr  
 385 390 395

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 Met Arg Ser  
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ccc	agc	gct	gct	tgg	ctg	ctg	ggg	gcc	atc	ctg	cta	gca	gcc	tct	106
Pro	Ser	Ala	Ala	Trp	Leu	Leu	Gly	Ala	Ala	Ile	Leu	Leu	Ala	Ala	Ser
5					10					15					

ctc	tcc	tgc	agt	ggc	acc	atc	caa	gga	acc	aat	aga	tcc	tct	aaa	gga	154
Leu	Ser	Cys	Ser	Gly	Thr	Ile	Gln	Gly	Thr	Asn	Arg	Ser	Ser	Lys	Gly	
20					25				30		35					

aga	agc	ctt	att	ggt	aag	gtt	gat	ggc	aca	tcc	cac	gtc	act	gga	aaa	202
Arg	Ser	Leu	Ile	Gly	Lys	Val	Asp	Gly	Thr	Ser	His	Val	Thr	Gly	Lys	
40						45				50						

gga	gtt	aca	gtt	gaa	aca	gtc	ttt	tct	gtg	gat	gag	ttt	tct	gca	tct	250
Gly	Val	Thr	Val	Glu	Thr	Val	Phe	Ser	Val	Asp	Glu	Phe	Ser	Ala	Ser	
55					60				65							

gtc	ctc	gct	gga	aaa	ctg	acc	act	gtc	tcc	ctt	cca	att	gtc	tac	aca	298
Val	Leu	Ala	Gly	Lys	Leu	Thr	Thr	Val	Phe	Leu	Pro	Ile	Val	Tyr	Thr	
70					75			80								

att	gtg	ttt	gct	gtg	ggt	ttg	cca	agt	aac	ggc	atg	gcc	cta	tgg	gtc	346
Ile	Val	Phe	Ala	Val	Gly	Leu	Pro	Ser	Asn	Gly	Met	Ala	Leu	Trp	Val	
85					90				95							

ttt	ctt	ttc	cga	act	aag	aag	cac	cct	gct	gtg	att	tac	atg	gcc	394
Phe	Leu	Phe	Arg	Thr	Lys	Lys	His	Pro	Ala	Val	Ile	Tyr	Met	Ala	
100					105				110		115				

aat	ctg	gcc	ttg	gct	gac	ctc	tct	gtc	atc	tgg	ttc	ccc	ttg	aag	442
Asn	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Ser	Val	Ile	Trp	Phe	Pro	Leu	Lys
					120				125		130				

att	gcc	tat	cac	ata	cat	ggc	aac	aac	tgg	att	tat	ggg	gaa	gct	ctt	490
Ile	Ala	Tyr	His	Ile	His	Gly	Asn	Asn	Trp	Ile	Tyr	Gly	Glu	Ala	Leu	
135					140					145						

tgt	aat	gtg	ctt	att	ggc	ttt	ttc	tat	cgc	aac	atg	tac	tgt	tcc	att	538
Cys	Asn	Val	Leu	Ile	Gly	Phe	Phe	Tyr	Gly	Asn	Met	Tyr	Cys	Ser	Ile	
150					155					160						

ctc	ttc	atg	acc	tgc	ctc	agt	gtg	cag	agg	tat	tgg	gtc	atc	gtg	aac	586
Leu	Phe	Met	Thr	Cys	Leu	Ser	Val	Gln	Arg	Tyr	Trp	Val	Ile	Val	Asn	
165					170					175						

ccc atg ggg cac tcc agg aag aag gca aac att gcc att ggc atc tcc		634	
Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala Ile Gly Ile Ser			
180	185	190	195
ctg gca ata tgg ctg ctg act ctg ctg gtc acc atc cct ttg tat gtc		682	
Leu Ala Ile Trp Leu Leu Thr Leu Leu Val Thr Ile Pro Leu Tyr Val			
200	205	210	
gtg aag cag acc atc ttc att cct gcc ctg aac atc acg acc tgt cat		730	
Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile Thr Thr Cys His			
215	220	225	
gat gtt ttg cct gag cag ctc ttg gtg gga gac atg ttc aat tac ttc		778	
Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met Phe Asn Tyr Phe			
230	235	240	
ctc tct ctg gcc att ggg gtc ttt ctg ttc cca gcc ttc ctc aca gcc		826	
Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Phe Leu Thr Ala			
245	250	255	
tct gcc tat gtg ctg atg atc aga atg ctg cga tct tct gcc atg gat		874	
Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser Ala Met Asp			
260	265	270	275
gaa aac tca gag aag aaa agg aag agg gcc atc aaa ctc att gtc act		922	
Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu Ile Val Thr			
280	285	290	
gtc ctg ggc atg tac ctg atc tgc ttc act cct agt aac ctt ctg ctt		970	
Val Leu Gly Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn Leu Leu Leu			
295	300	305	
gtg gtg cat tat ttt ctg att aag agc cag ggc cag agc cat gtc tat		1018	
Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln Ser His Val Tyr			
310	315	320	
gcc ctg tac att gta gcc ctc tgc ctc tct acc ctt aac agc tgc atc		1066	
Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys Ile			
325	330	335	
gac ccc ttt gtc tat tac ttt gtt tca cat gat ttc agg gat cat gca		1114	
Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg Asp His Ala			
340	345	350	355
aag aac gct ctc ctt tgc cga agt gtc cgc act gta aag cag atg caa		1162	
Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys Gln Met Gln			
360	365	370	
gta ccc ctc acc tca aag aaa cac tcc agg aaa tcc agc tct tac tct		1210	
Val Pro Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser Tyr Ser			
375	380	385	
tca agt tca acc act gtt aag acc tcc tat tgagtttcc aggtcctcag		1260	
Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr			
390	395		
atggaaattg cacagtagga tgtggaacct gtttatgtt atgaggacgt gtctgttatt		1320	

tccggatcca gatcttatta aagcagaact tgtttattgc agcttataat ggttacaaat 1380  
aaagcaatag catcacaaat ttcacaaata aagc 1414

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<211> 397  
<212> PRT  
<213> Homo sapiens

<400> 63  
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Ala Ala Ser Leu Ser Cys Ser Gly Thr Ile Gln Gly Thr Asn Arg Ser  
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Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val  
35 40 45  
Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe  
50 55 60  
Ser Ala Ser Val Leu Ala Gly Lys Leu Thr Thr Val Phe Leu Pro Ile  
65 70 75 80  
Val Tyr Thr Ile Val Phe Ala Val Gly Leu Pro Ser Asn Gly Met Ala  
85 90 95  
Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile  
100 105 110  
Tyr Met Ala Asn Leu Ala Leu Asp Leu Leu Ser Val Ile Trp Phe  
115 120 125  
Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr Gly  
130 135 140  
Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr  
145 150 155 160  
Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val  
165 170 175  
Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala Ile  
180 185 190  
Gly Ile Ser Leu Ala Ile Trp Leu Leu Thr Leu Leu Val Thr Ile Pro  
195 200 205  
Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile Thr  
210 215 220  
Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met Phe  
225 230 235 240  
Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Phe  
245 250 255

Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser  
260 265 270

Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu  
275 280 285

Ile Val Thr Val Leu Gly Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn  
290 295 300

Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln Ser  
305 310 315 320

His Val Tyr Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu Asn  
325 330 335

Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg  
340 345 350

Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys  
355 360 365

Gln Met Gln Val Pro Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser  
370 375 380

Ser Tyr Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr  
385 390 395